REMARKS

Sequence Compliance

Applicants have amended the specification and drawings to define all sequences therein.

Drawings

Applicants submit herewith replacement drawings for Figures 15 and 16.

Rejection of Claims and Traversal Thereof

In the April 8, 2010 Office Action:

Claim 25 was rejected under 35 U.S.C. §112, second paragraph;

Claims 10, 21, 23, 25, 26, and 28 were rejected under 35 U.S.C. §112, first paragraph; and

Claims 10, 21-24, 27 and 28 were rejected under 35 U.S.C. §102(b) as being anticipated by WO 02/060492.

These rejections are hereby traversed and reconsideration of the patentability of the pending claims is therefore requested in light of the following remarks.

Rejection under 35 U.S.C. §112, second paragraph

Claim 25 was rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicants regard as the invention. Applicants have amended claim 25 thereby obviating this rejection. Withdrawal of this rejection is requested.

Rejection under 35 U.S.C. §112, first paragraph

Claims 10, 21, 23, 25, 26, and 28 were rejected under 35 U.S.C. §112, first paragraph for numerous reasons, each of which is addressed hereinbelow.

Claim 10 was amended to meet all requirements of section 112, first paragraph.

Claim 21 was amended to clearly define the step required to identify binding partners and if such binding partners affect the activity of the Futrin 2 polypeptide, as set forth below:

- 21. A method of identifying a binding partner for a Futrin 2 polypeptide that affects the activity of the polypeptide, the method comprising
- (a) contacting said Futrin 2 polypeptide with a compound to be screened; and
- (b) determining if binding of the compound to the Futrin 2 has occurred thereby forming a Futrin 2/ binding partner complex; and
- (c) assaying the Futrin 2/binding partner complex to determine if the binding partner affects the activity of the futrin 2 polypeptide.

Support for the amendment to claim 21 can be found on the bottom of page 20 and top of page 21. Applicants have provided numerous assays to determine the activity of the Futrin 2 after binding with the binding partner, such as found on page 21, third paragraph. Due to the amendment of claim 21, claims 23, 25, 26and 28 now meet all requirements of section 112. Applicants request withdrawal of all rejections relating to enablement, written description and new matter.

Rejection under 35 U.S.C. §102(b)

Claims 10, 21-24, 27 and 28 were rejected under 35 U.S.C. §102(b) as being anticipated by Warren et al. (US Patent Publication No: 2004/0077048). Applicants submit that the cited reference does not anticipate the presently claimed invention.

To anticipate a claim, a reference must:

- 1) disclose each and every limitation of the claimed invention;
- 2) be enabling; and
- 3) describe the claimed invention sufficiently to place it in possession of a person of ordinary skill in the field of the invention

Helifix Ltd. v. Blok-Lok, Ltd., 54 USPQ2d 1299 (Fed. Cir. 2000).

According to the Office, the sequence listing set forth in the Warren reference is the same as that of applicants' SEQ ID NO. 26. Applicants vigorously disagree because when Sequence 12 of the cited reference is compared to that of SEQ ID NO. 26 of the present invention it is very evident that the sequences are not the same, as shown below. Notably, the change of two amino acid residues is sufficient to introduce the possibility of changing the tertiary structure and thus any interaction with binding partners. Thus, each and every limitation of the claimed invention is not disclosed.

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>lcl{13559 unnamed protein product
Length=243

Score = 498 bits (1281), Expect = 7e-146, Method: Compositional matrix adjust.
Identities = 241/243 (998), Positives = 241/243 (998), Gaps = 0/243 (0%)

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MQFRLFSFALIILNCMDYSHCQGNRWRRSHRASYVSNPICKGCLSCSKDNGCSRCQQRLF
MQFRLFSFALIILNCMDYSHCQGNRWRRSKRASYVSNPICKGCLSCSKDNGCSRCQQRLF
Suery
                                                                                                           60
                                                                                                           60
                MOTPLFSFALIILNONDYSHOOGNEWERSKRASİVSNPICKBOLSUSKDNGUSECQQKLF
                 FFLRREGMROYGECLHSCPSGYYGHRAPDMNRCARCRIENCDSCFSKDFCTRCKVGFYLH
FFLRREGMROYGECLHSCPSGYYGHRAPDMNRCARCRIENCDSCFSKDFCTRCKVGFYLH
Query
                 fflrregnroygeolhscrsgyyghrapinnrcarcriencdscfskdrotkckygfylh
Sbjat
                                                                                                           120
Query
                      :FDECPDGFAPLEETMECVEG:EVGHWSEWGTCSRNNRTOGFKWGLETRTBQIVKKP
| FDECPDGFAPLEETMECVEGCEVGHWSEWGTCSRNNRTOGFKWGLETRTRQIVKKP
                                                                                                           180
          323
35iot
          121
                 egrsfdecpdgfapleetmecvegcevghwsewgtcsrnnrtcgfkwgletrtrqivekp
                 vkdtipcptiaesrckmimrhcpggrripkakekrnknnrkliepageghsvalatdr
vkdtipcptiaesrckmimrhcpggkripkakekrnkkkkrklierage asvflatdr
Cuery
                                                                                                           240
Sbjot
                VEDTIECPTIAESBECENTMBHCPGGKRTPRAKEKBNKKKRKLIERAÇEGHSVFLATDR
                                                                                                          240
          191
Query
                ANO
                        243
                 ANO
Sbjet
          241
                        243
                 CMA
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Clearly, the sequence used in the Warren reference is not Futrin 2, and as such, how can such an unknown sequence be the equivalent of Futrin 2 with the same capabilities of modulating the Wnt pathway. Notably the Warren reference never addresses the Futrin 2 protein and instead describes the Sequence 12, as follows:

As another example, SEQ ID NO: 12 is 43% identical (over 204 amino acid residues) to a murine thrombospondin type 1 domain (GenBank ID g4519541), characteristic of the ADAMTS metalloproteinases family, as determined by the Basic Local Alignment Search Tool (BLAST). (See Table 2.) The BLAST probability score is 9.4e⁻⁴⁹, which indicates the probability of obtaining the observed polypeptide sequence alignment by chance. SEQ ID NO: 12 also shares 30% identity (over 183 amino acid residues) with a Spodoptera frugiperda endoprotease (GenBank ID gll67860), with a BLAST probability score of 7. 3 e⁻¹⁰

The Warren reference provides human protein modification and maintenance molecules (PMMM) and polynucleotides which identify and encode PMMM. However this reference does not sufficiently describe the present invention to place it in possession of a person of ordinary skill in the field of the invention and thus is not an anticipatory reference. Applicants request that this rejection for lack of novelty be withdrawn.

Petition for Extension and Fees Payable

Applicants petition for a two month extension to extend the response due date of July 8, 2010 to September 8, 2010 and the fee for a large entity is being paid herewith by electronic transfer. If any additional fee is found due for entry of this amendment, the Commissioner is authorized to charge such fee to Deposit Account No. 13-4365 of Moore & Van Allen.

Conclusion

Applicants have satisfied the requirements for patentability. All pending claims are free of the art and fully comply with the requirements of 35 U.S.C. §112. It therefore is requested that Examiner Marvich reconsider the patentability of the pending claims in light of the distinguishing remarks herein, and withdraw all rejections, thereby placing the application in condition for allowance. If any issues remain outstanding incident to the allowance of the application, Examiner Marvich is requested to contact the undersigned attorney at (919) 286-8089.

Respectfully submitted,

/mariannefuierer/

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